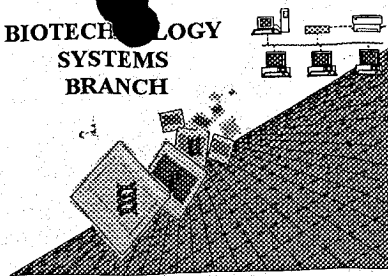


Nelson

File Copy

#25

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/446,089C

Source: 1638 RustA

Date Processed by STIC: 6/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/446 089C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 10 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (Sec "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1638

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001
TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\06202001\I446089C.raw

Does Not Comply
Corrected Diskette Needed

pr 5-6

3 <110> APPLICANT: SAKAKIBARA, Keiko
4 FUKUI, Yuko
5 TANAKA, Yoshikazu
6 KUSUMI, Takaaki
7 MIZUTANI, Masako
8 NAKAYAMA, Toru
10 <120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY
12 <130> FILE REFERENCE: 001560-377
14 <140> CURRENT APPLICATION NUMBER: US 09/446,089C
15 <141> CURRENT FILING DATE: 1999-12-17
17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02045
18 <151> PRIOR FILING DATE: 1999-04-16
20 <150> PRIOR APPLICATION NUMBER: JP 10/107296
21 <151> PRIOR FILING DATE: 1998-04-17
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1951
29 <212> TYPE: DNA
30 <213> ORGANISM: Antirrhinum majus
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (96)..(1781)
36 <400> SEQUENCE: 1
37 aaattacatt gcttcctttg tcccaccttc caccaccaat atatacaact tcctcagcta 60
39 gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat 113
40 Met Phe Lys Asn Pro Asn
41 1 5
43 atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161
44 Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
45 10 15 20
47 tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209
48 Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
49 25 30 35
51 cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257
52 Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
53 40 45 50
55 ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305
56 Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
57 55 60 65 70
59 tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt 353
60 Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
61 75 80 85
63 ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc 401
64 Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
65 90 95 100
67 act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac 449

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001

TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\06202001\I446089C.raw

68	Thr	Thr	Met	Arg	Val	Arg	Arg	Ala	Ala	His	Leu	Val	Asp	Asp	Ala	Tyr	
69			105					110					115				
71	att	gcc	aaa	ttc	aag	aaa	gcc	gtt	gag	ctt	atg	cga	gct	cta	cct	gag	497
72	Ile	Ala	Lys	Phe	Lys	Lys	Ala	Val	Glu	Leu	Met	Arg	Ala	Leu	Pro	Glu	
73		120					125					130					
75	gat	gac	cct	cgt	agc	ttc	aag	caa	caa	gct	aac	gtc	cat	tgc	gct	tac	545
76	Asp	Asp	Pro	Arg	Ser	Phe	Lys	Gln	Gln	Ala	Asn	Val	His	Cys	Ala	Tyr	
77	135					140					145				150		
79	tgc	gcg	ggg	gcg	tat	aat	caa	gcc	ggg	ttc	aca	aac	cta	aag	ctc	caa	593
80	Cys	Ala	Gly	Ala	Tyr	Asn	Gln	Ala	Gly	Phe	Thr	Asn	Leu	Lys	Leu	Gln	
81					155					160					165		
83	atc	cac	cga	tct	tgg	ctt	ttt	ttc	ccg	ttc	cat	aga	tat	tat	atc	tac	641
84	Ile	His	Arg	Ser	Trp	Leu	Phe	Phe	Pro	Phe	His	Arg	Tyr	Tyr	Ile	Tyr	
85			170					175					180				
87	ttt	ttt	gaa	aga	ata	ttg	gga	aaa	cta	atc	aat	gat	aca	act	ttt	gct	689
88	Phe	Phe	Glu	Arg	Ile	Leu	Gly	Lys	Leu	Ile	Asn	Asp	Thr	Thr	Phe	Ala	
89			185				190					195					
91	ctc	caa	ttt	tgg	aac	tat	gat	tca	cct	ggg	gga	atg	aca	atc	cca	tca	737
92	Leu	Gln	Phe	Trp	Asn	Tyr	Asp	Ser	Pro	Gly	Gly	Met	Thr	Ile	Pro	Ser	
93		200				205					210						
95	atg	ttt	att	gat	act	aat	tct	tgc	ctg	tac	gat	agt	tta	cgg	gac	agt	785
96	Met	Phe	Ile	Asp	Thr	Asn	Ser	Ser	Leu	Tyr	Asp	Ser	Leu	Arg	Asp	Ser	
97	215				220				225				230				
99	aat	cat	cag	cca	cca	acc	atc	gta	gac	ttg	aac	tac	gcc	ttt	tct	gat	833
100	Asn	His	Gln	Pro	Pro	Thr	Ile	Val	Asp	Leu	Asn	Tyr	Ala	Phe	Ser	Asp	
101				235				240				245					
103	tcc	gac	aat	acc	act	act	cct	gaa	gag	caa	atg	att	ata	aac	ctt	aaa	881
104	Ser	Asp	Asn	Thr	Thr	Thr	Pro	Glu	Glu	Gln	Met	Ile	Ile	Asn	Leu	Lys	
105			250					255				260					
107	att	gtg	tac	aga	caa	atg	gtg	tgc	agc	gct	aag	act	cca	cag	ctt	ttc	929
108	Ile	Val	Tyr	Arg	Gln	Met	Val	Ser	Ser	Ala	Lys	Thr	Pro	Gln	Leu	Phe	
109			265				270					275					
111	ttc	ggc	cgc	cca	tac	cga	cgt	ggg	gac	caa	gag	ttt	ccc	ggg	gtg	ggg	977
112	Phe	Gly	Arg	Pro	Tyr	Arg	Arg	Gly	Asp	Gln	Glu	Phe	Pro	Gly	Val	Gly	
113		280				285					290						
115	tgc	att	gag	tta	gtc	cct	cat	ggc	atg	ata	cat	tta	tgg	acc	ggg	tct	1025
116	Ser	Ile	Glu	Leu	Val	Pro	His	Gly	Met	Ile	His	Leu	Trp	Thr	Gly	Ser	
117	295				300				305				310				
119	gag	aac	acg	ccc	tat	ggc	gag	aac	atg	ggg	gct	ttc	tac	tca	acg	gct	1073
120	Glu	Asn	Thr	Pro	Tyr	Gly	Glu	Asn	Met	Gly	Ala	Phe	Tyr	Ser	Thr	Ala	
121				315				320				325					
123	aga	gac	cgc	ata	ttt	ttt	gct	cat	cat	tgc	aac	gtc	gat	aga	atg	tgg	1121
124	Arg	Asp	Pro	Ile	Phe	Phe	Ala	His	His	Ser	Asn	Val	Asp	Arg	Met	Trp	
125			330				335					340					
127	tcc	ata	tgg	aag	acc	cta	gga	ggg	cgc	cgg	agg	acg	gac	tta	aca	gat	1169
128	Ser	Ile	Trp	Lys	Thr	Leu	Gly	Gly	Pro	Arg	Arg	Thr	Asp	Leu	Thr	Asp	
129		345				350					355						
131	cca	gat	ttt	ctt	gat	gcg	tct	ttc	gtt	ttt	tat	gac	gaa	aac	gca	gag	1217
132	Pro	Asp	Phe	Leu	Asp	Ala	Ser	Phe	Val	Phe	Tyr	Asp	Glu	Asn	Ala	Glu	

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/446,089C

TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\06202001\I446089C.raw

```

133      360      365      370
135 atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg      1265
136 Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
137 375      380      385      390
139 tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca      1313
140 Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
141      395      400      405
143 cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act      1361
144 Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
145      410      415      420
147 gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa      1409
148 Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
149      425      430      435
151 gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac      1457
152 Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
153      440      445      450
155 gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac      1505
156 Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
157 455      460      465      470
159 cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac      1553
160 His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
161      475      480      485
163 ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg      1601
164 Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
165      490      495      500
167 agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta      1649
168 Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
169      505      510      515
171 tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa      1697
172 Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
173      520      525      530
175 gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg      1745
176 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
177 535      540      545      550
179 atc aag att cat aat gtc aag att gag ctt gat ggc taataaatto      1791
180 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
181      555      560
183 tattgatttc ttctcaacct acagttgatc atttaccgat tgattattoc aataaaagta      1851
185 tctcatgtac caatatcgat cgtattaatc gtaatacttt cagattttta tttatttaaa      1911
187 agcagttgta taaatggtga aataaggatt actttttgag      1951
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 562
192 <212> TYPE: PRT
193 <213> ORGANISM: Antirrhinum majus
195 <400> SEQUENCE: 2
197 Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser
198 1      5      10      15
201 Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu
202      20      25      30

```

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/446,089C

TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\06202001\I446089C.raw

```

205 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
206          35          40          45
209 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
210          50          55          60
213 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
214 65          70          75          80
217 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
218          85          90          95
221 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
222          100          105          110
225 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
226          115          120          125
229 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
230          130          135          140
233 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
234 145          150          155          160
237 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
238          165          170          175
241 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
242          180          185          190
245 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
246          195          200          205
249 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
250          210          215          220
253 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
254 225          230          235          240
257 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
258          245          250          255
261 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
262          260          265          270
265 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
266          275          280          285
269 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
270          290          295          300
273 His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
274 305          310          315          320
277 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
278          325          330          335
281 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
282          340          345          350
285 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
286          355          360          365
289 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
290          370          375          380
293 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
294 385          390          395          400
297 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
298          405          410          415
301 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile

```

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/446,089C

TIME: 11:02:47

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\06202001\I446089C.raw

```

302          420          425          430
305 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
306          435          440          445
309 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
310          450          455          460
313 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
314 465          470          475          480
317 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
318          485          490          495
321 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
322          500          505          510
325 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
326          515          520          525
329 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
330          530          535          540
333 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
334 545          550          555          560
337 Asp Gly

```

341 <210> SEQ ID NO: 3

342 <211> LENGTH: 13

343 <212> TYPE: PRT

344 <213> ORGANISM: Antirrhinum majus

346 <400> SEQUENCE: 3

348 Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro

349 1 5 10

352 <210> SEQ ID NO: 4

353 <211> LENGTH: 12

354 <212> TYPE: PRT

355 <213> ORGANISM: Antirrhinum majus

357 <400> SEQUENCE: 4

359 Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys

360 1 5 10

362 <210> SEQ ID NO: 5

363 <211> LENGTH: 18

364 <212> TYPE: PRT

365 <213> ORGANISM: Antirrhinum majus

367 <400> SEQUENCE: 5

369 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln

370 1 5 10 15

372 Glu Phe

375 <210> SEQ ID NO: 6

376 <211> LENGTH: 29

377 <212> TYPE: PRT

378 <213> ORGANISM: Antirrhinum majus

380 <220> FEATURE:

381 <221> NAME/KEY: UNSURE

382 <222> LOCATION: (8)..(8)

383 <223> OTHER INFORMATION: Amino acid 8 is Xaa wherein Xaa = unknown or other.

385 <220> FEATURE:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

09/446,089C 6

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

see item 11 on Enr Summary Sheet

<400> 10

His Ala Val Cys Asn Glu

1

5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/446,089C

DATE: 06/20/2001

TIME: 11:02:48

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\06202001\I446089C.raw

L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:466 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:466 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13